

## Blast Result

EXHIBIT 6



## Blast 2 Sequences results

Entrez

BLAST

OMIM

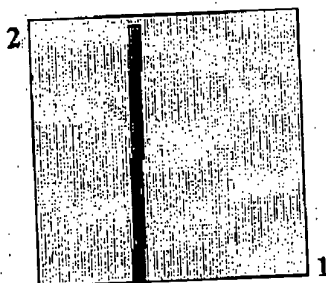
Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 gi Homo sapiens endothelial differentiation, sphingolipid G- Length 1137 (1..1137)  
 488..194 protein-coupled receptor, 3 (EDG3), mRNA  
 Sequence 2 icl|s:q\_2 Length 23 (1..23)  
 2



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 44.9 bits (23), Expect = 0.17  
 Identities = 23/23 (100%)  
 Strand = Plus / Plus

Query: 423 caaaatgaggccttacgacgcc 445

Sbjct: 1 caaaatgaggccttacgacgcc 23

CPU time: 0.05 user secs. 0.13 sys. secs. 0.18 total secs.

Lambda K H  
 1.33 0.621 1.12

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 1

3/8/2002

## Blast Result

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Number of Sequences: 0  
Number of extensions: 1  
Number of successful extensions: 1  
Number of sequences better than 10:0: 1  
length of query: 1137  
length of database: 5,006,917,935  
effective HSP length: 24  
effective length of query: 1113  
effective length of database: 4,991,889,975  
effective search space: 5555973542175  
effective search space used: 5555973542175  
T: 0  
A: 30  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 20 (39.1 bits)